



SEQUENCE LISTING

<110> Pagano, M.

<120> METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

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<140> 10/042,417

<141> 2002-01-07

<150> 60/260,179

<151> 2001-01-05

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<170> PatentIn Ver. 2.0

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Lys Tyr Leu Pro Leu Leu Asp Arg Ala His Ala Ser Gln Val Cys Arg
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Asn Trp Asn Gln Val Phe His Met Pro Asp Leu Trp Arg Cys Phe Glu
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Phe Glu Leu Asn Gln Pro Ala Thr Ser Tyr Leu Lys Ala Thr His Pro
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Glu Leu Ile Lys Gln Ile Ile Lys Arg His Ser Asn His Leu Gln Tyr
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Gln Leu Gly Ser Thr Asn His Tyr Trp Asn Glu Thr Val Arg Asn Pro
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Ile Leu Trp Arg Tyr Phe Leu Leu Arg Asp Leu Pro Ser Trp Ser Ser
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Val Asp Trp Lys Ser Leu Pro Tyr Leu Gln Ile Leu Lys Lys Pro Ile
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<211> 447
<212> PRT
<213> Homo sapiens

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Ser Asp Ser Cys Lys Glu Glu Ser Ser Thr Leu Ser Val Lys Met Lys
35 40 45

Cys Asp Phe Asn Cys Asn His Val His Ser Gly Leu Lys Leu Val Lys
50 55 60

Pro Asp Asp Ile Gly Arg Leu Val Ser Tyr Thr Pro Ala Tyr Leu Glu
65 70 75 80

Gly Ser Cys Lys Asp Cys Ile Lys Asp Tyr Glu Arg Leu Ser Cys Ile
 85 90 95

 Gly Ser Pro Ile Val Ser Pro Arg Ile Val Gln Leu Glu Thr Glu Ser
 100 105 110

 Lys Arg Leu His Asn Lys Glu Asn Gln His Val Gln Gln Thr Leu Asn
 115 120 125

 Ser Thr Asn Glu Ile Glu Ala Leu Glu Thr Ser Arg Leu Tyr Glu Asp
 130 135 140

 Ser Gly Tyr Ser Ser Phe Ser Leu Gln Ser Gly Leu Ser Glu His Glu
 145 150 155 160

 Glu Gly Ser Leu Leu Glu Glu Asn Phe Gly Asp Ser Leu Gln Ser Cys
 165 170 175

 Leu Leu Gln Ile Gln Ser Pro Asp Gln Tyr Pro Asn Lys Asn Leu Leu
 180 185 190

 Pro Val Leu His Phe Glu Lys Val Val Cys Ser Thr Leu Lys Lys Asn
 195 200 205

 Ala Lys Arg Asn Pro Lys Val Asp Arg Glu Met Leu Lys Glu Ile Ile
 210 215 220

 Ala Arg Gly Asn Phe Arg Leu Gln Asn Ile Ile Gly Arg Lys Met Gly
 225 230 235 240

 Leu Glu Cys Val Asp Ile Leu Ser Glu Leu Phe Arg Arg Gly Leu Arg
 245 250 255

 His Val Leu Ala Thr Ile Leu Ala Gln Leu Ser Asp Met Asp Leu Ile
 260 265 270

 Asn Val Ser Lys Val Ser Thr Thr Trp Lys Lys Ile Leu Glu Asp Asp
 275 280 285

 Lys Gly Ala Phe Gln Leu Tyr Ser Lys Ala Ile Gln Arg Val Thr Glu
 290 295 300

 Asn Asn Asn Lys Phe Ser Pro His Ala Ser Thr Arg Glu Tyr Val Met
 305 310 315 320

 Phe Arg Thr Pro Leu Ala Ser Val Gln Lys Ser Ala Ala Gln Thr Ser
 325 330 335

 Leu Lys Lys Asp Ala Gln Thr Lys Leu Ser Asn Gln Gly Asp Gln Lys
 340 345 350

 Gly Ser Thr Tyr Ser Arg His Asn Glu Phe Ser Glu Val Ala Lys Thr
 355 360 365

 Leu Lys Lys Asn Glu Ser Leu Lys Ala Cys Ile Arg Cys Asn Ser Pro
 370 375 380

 Ala Lys Tyr Asp Cys Tyr Leu Gln Arg Ala Thr Cys Lys Arg Glu Gly
 385 390 395 400

Cys Gly Phe Asp Tyr Cys Thr Lys Cys Leu Cys Asn Tyr His Thr Thr
405 410 415

Lys Asp Cys Ser Asp Gly Lys Leu Leu Lys Ala Ser Cys Lys Ile Gly
420 425 430

Pro Leu Pro Gly Thr Lys Lys Ser Lys Lys Asn Leu Arg Arg Leu
435 440 445

<210> 11
<211> 1535
<212> DNA
<213> Homo sapiens

<400> 11

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<210> 12

<211> 338

<212> PRT

<213> Homo sapiens

<400> 12

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Val Leu Ser Arg Pro Pro Pro Gly Gly Gly Asp Ser Phe Arg Thr Arg
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Arg Pro Gln Arg Gly Pro Gly Pro Gly Ser Gln Ala Met Asp Ala
35 40 45

Pro His Ser Lys Ala Ala Leu Asp Ser Ile Asn Glu Leu Pro Asp Asn
50 55 60

Ile Leu Leu Glu Leu Phe Thr His Val Pro Ala Arg Gln Leu Leu Leu
 65 70 75 80
 Asn Cys Arg Leu Val Cys Ser Leu Trp Arg Asp Leu Ile Asp Leu Leu
 85 90 95
 Thr Leu Trp Lys Arg Lys Cys Leu Arg Lys Gly Phe Ile Thr Lys Asp
 100 105 110
 Trp Asp Gln Pro Val Ala Asp Trp Lys Ile Phe Tyr Phe Leu Arg Ser
 115 120 125
 Leu His Arg Asn Leu Leu Arg Asn Pro Cys Ala Glu Asn Asp Met Phe
 130 135 140
 Ala Trp Gln Ile Asp Phe Asn Gly Gly Asp Arg Trp Lys Val Asp Ser
 145 150 155 160
 Leu Pro Gly Ala His Gly Thr Glu Phe Pro Asp Pro Lys Val Lys Lys
 165 170 175
 Ser Phe Val Thr Ser Tyr Glu Leu Cys Leu Lys Trp Glu Leu Val Asp
 180 185 190
 Leu Leu Ala Asp Arg Tyr Trp Glu Glu Leu Leu Asp Thr Phe Arg Pro
 195 200 205
 Asp Ile Val Val Lys Asp Trp Phe Ala Ala Arg Ala Asp Cys Gly Cys
 210 215 220
 Thr Tyr Gln Leu Lys Val Gln Leu Ala Ser Ala Asp Tyr Phe Val Leu
 225 230 235 240
 Ala Ser Phe Glu Pro Pro Pro Val Thr Ile Gln Gln Trp Asn Asn Ala
 245 250 255
 Thr Trp Thr Glu Val Ser Tyr Thr Phe Ser Asp Tyr Pro Arg Gly Val
 260 265 270
 Arg Tyr Ile Leu Phe Gln His Gly Gly Arg Asp Thr Gln Tyr Trp Ala
 275 280 285
 Gly Trp Tyr Gly Pro Arg Val Thr Asn Ser Ser Ile Val Val Ser Pro
 290 295 300
 Lys Met Thr Arg Asn Gln Ala Ser Ser Glu Ala Gln Pro Gly Gln Lys
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 His Gly Gln Glu Glu Ala Ala Gln Ser Pro Tyr Gly Ala Val Val Gln
 325 330 335
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<210> 13
 <211> 1763
 <212> DNA
 <213> Homo sapiens

<400> 13

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 <211> 482
 <212> PRT
 <213> Homo sapiens

<400> 14															
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Leu	Ile	Cys	Leu	Ile	Leu	His	Asp	Asp	Ile	Pro	Pro	Pro	Asn	Ile	Pro
														45	
Ser	Ser	Thr	Asp	Ser	Glu	His	Ser	Ser	Leu	Gln	Asn	Asn	Glu	Gln	Pro
														60	
Ser	Leu	Ala	Thr	Ser	Ser	Asn	Gln	Thr	Ser	Ile	Gln	Asp	Glu	Gln	Pro
														80	
Ser	Asp	Ser	Phe	Gln	Gly	Gln	Ala	Ala	Gln	Ser	Gly	Val	Trp	Asn	Asp
														95	
Asp	Ser	Met	Leu	Gly	Pro	Ser	Gln	Asn	Phe	Glu	Ala	Glu	Ser	Ile	Gln
														110	
Asp	Asn	Ala	His	Met	Ala	Glu	Gly	Thr	Gly	Phe	Tyr	Pro	Ser	Glu	Pro
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Leu Leu Cys Ser Glu Ser Val Glu Gly Gln Val Pro His Ser Leu Glu
 130 135 140

Thr Leu Tyr Gln Ser Ala Asp Cys Ser Asp Ala Asn Asp Ala Leu Ile
 145 150 155 160

Val Leu Ile His Leu Leu Met Leu Glu Ser Gly Tyr Ile Pro Gln Gly
 165 170 175

Thr Glu Ala Lys Ala Leu Ser Leu Pro Glu Lys Trp Lys Leu Ser Gly
 180 185 190

Val Tyr Lys Leu Gln Tyr Met His His Leu Cys Glu Gly Ser Ser Ala
 195 200 205

Thr Leu Thr Cys Val Pro Leu Gly Asn Leu Ile Val Val Asn Ala Thr
 210 215 220

Leu Lys Ile Asn Asn Glu Ile Arg Ser Val Lys Arg Leu Gln Leu Leu
 225 230 235 240

Pro Glu Ser Phe Ile Cys Lys Glu Lys Leu Gly Glu Asn Val Ala Asn
 245 250 255

Ile Tyr Lys Asp Leu Gln Lys Leu Ser Arg Leu Phe Lys Asp Gln Leu
 260 265 270

Val Tyr Pro Leu Leu Ala Phe Thr Arg Gln Ala Leu Asn Leu Pro Asn
 275 280 285

Val Phe Gly Leu Val Val Leu Pro Leu Glu Leu Lys Leu Arg Ile Phe
 290 295 300

Arg Leu Leu Asp Val Arg Ser Val Leu Ser Leu Ser Ala Val Cys Arg
 305 310 315 320

Asp Leu Phe Thr Ala Ser Asn Asp Pro Leu Leu Trp Arg Phe Leu Tyr
 325 330 335

Leu Arg Asp Phe Arg Asp Asn Thr Val Arg Val Gln Asp Thr Asp Trp
 340 345 350

Lys Glu Leu Tyr Arg Lys Arg His Ile Gln Arg Lys Glu Ser Pro Lys
 355 360 365

Gly Arg Phe Val Leu Leu Leu Pro Ser Ser Thr His Thr Ile Pro Phe
 370 375 380

Tyr Pro Asn Pro Leu His Pro Arg Pro Phe Pro Ser Ser Arg Leu Pro
 385 390 395 400

Pro Gly Ile Ile Gly Gly Glu Tyr Asp Gln Arg Pro Thr Leu Pro Tyr
 405 410 415

Val Gly Asp Pro Ile Ser Ser Leu Ile Pro Gly Pro Gly Glu Thr Pro
 420 425 430

Ser Gln Leu Pro Pro Leu Arg Pro Arg Phe Asp Pro Val Gly Pro Leu
 435 440 445

Pro Gly Pro Asn Pro Ile Leu Pro Gly Arg Gly Gly Pro Asn Asp Arg
450 455 460

Phe Pro Phe Arg Pro Ser Arg Gly Arg Pro Thr Asp Gly Arg Leu Ser
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Phe Met

<210> 15
<211> 43
<212> PRT
<213> Homo sapiens

<400> 15
Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr
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Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys Lys Glu Trp
20 25 30

Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys
35 40

<210> 16
<211> 40
<212> PRT
<213> Homo sapiens

<400> 16
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1 5 10 15

Thr Leu Leu Thr Cys Cys Leu Val Ser Lys Gln Trp Asn Lys Val Ile
20 25 30

Ser Ala Cys Thr Glu Val Trp Gln
35 40

<210> 17
<211> 39
<212> PRT
<213> Homo sapiens

<400> 17
Leu Leu Gln Asp Ile Ile Leu Gln Val Phe Lys Tyr Leu Pro Leu Leu
1 5 10 15

Asp Arg Ala His Ala Ser Gln Val Cys Arg Asn Trp Asn Gln Val Phe
20 25 30

His Met Pro Asp Leu Trp Arg
35

<210> 18
<211> 39

<212> PRT
 <213> Homo sapiens

<400> 18
 Leu Pro Ile Asp Val Gln Leu Tyr Ile Leu Ser Phe Leu Ser Pro His
 1 5 10 15

Asp Leu Cys Gln Leu Gly Ser Thr Asn His Tyr Trp Asn Glu Thr Val
 20 25 30

Arg Asn Pro Ile Leu Trp Arg
 35

<210> 19
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 19
 Leu Arg His Val Leu Ala Thr Ile Leu Ala Gln Leu Ser Asp Met Asp
 1 5 10 15

Leu Ile Asn Val Ser Lys Val Ser Thr Thr Trp Lys Lys Ile Leu Glu
 20 25 30

Asp Asp Lys Gly Ala Phe Gln
 35

<210> 20
 <211> 40
 <212> PRT
 <213> Homo sapiens

<400> 20
 Leu Pro Asp Asn Ile Leu Leu Glu Leu Phe Thr His Val Pro Ala Arg
 1 5 10 15

Gln Leu Leu Leu Asn Cys Arg Leu Val Cys Ser Leu Trp Arg Asp Leu
 20 25 30

Ile Asp Leu Leu Thr Leu Trp Lys
 35 40

<210> 21
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 21
 Leu Pro Leu Glu Leu Lys Leu Arg Ile Phe Arg Leu Leu Asp Val Arg
 1 5 10 15

Ser Val Leu Ser Leu Ser Ala Val Cys Arg Asp Leu Phe Thr Ala Ser
 20 25 30

Asn Asp Pro Leu Leu Trp Arg
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<210> 22
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 22
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Glu Leu Leu Lys Val Ser Gly Val Cys Lys Arg Trp Tyr Arg Leu Ala
 20 25 30

Ser Asp Glu Ser Leu Trp Gln
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<210> 23
 <211> 1323
 <212> DNA
 <213> Homö sapiens

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<210> 24
 <211> 434
 <212> PRT
 <213> Homo sapiens

<400> 24
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Gly Ala Ala Lys Gln Pro Lys Val Glu Phe Tyr Ser Ser Leu Asn Gln
 20 25 30

Thr His Thr His Thr Val Leu Leu Asp Trp Gly Ser Leu Pro His His
 35 40 45

Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu Asp Arg Ala Cys
 50 55 60

Ala Ser Ser Val Cys Arg Arg Trp Asn Glu Val Phe His Ile Ser Asp
 65 70 75 80

Leu Trp Arg Lys Phe Glu Phe Glu Leu Asn Gln Ser Ala Thr Ser Ser
 85 90 95

Phe Lys Ser Thr His Pro Asp Leu Ile Gln Gln Ile Ile Lys Lys His
 100 105 110

Phe Ala His Leu Gln Tyr Val Ser Phe Lys Val Asp Ser Ser Ala Glu
 115 120 125

Ser Ala Glu Ala Ala Cys Asp Ile Leu Ser Gln Leu Val Asn Cys Ser
 130 135 140

Ile Gln Thr Leu Gly Leu Ile Ser Thr Ala Lys Pro Ser Phe Met Asn
 145 150 155 160

Val Ser Glu Ser His Phe Val Ser Ala Leu Thr Val Val Phe Ile Asn
 165 170 175

Ser Lys Ser Leu Ser Ser Ile Lys Ile Glu Asp Thr Pro Val Asp Asp
 180 185 190

Pro Ser Leu Lys Ile Leu Val Ala Asn Asn Ser Asp Thr Leu Arg Leu
 195 200 205

Pro Lys Met Ser Ser Cys Pro His Val Ser Ser Asp Gly Ile Leu Cys
 210 215 220

Val Ala Asp Arg Cys Gln Gly Leu Arg Glu Leu Ala Leu Asn Tyr Tyr
 225 230 235 240

Ile Leu Thr Asp Glu Leu Phe Leu Ala Leu Ser Ser Glu Thr His Val
 245 250 255

Asn Leu Glu His Leu Arg Ile Asp Val Val Ser Glu Asn Pro Gly Gln
 260 265 270

Ile Lys Phe His Ala Val Lys Lys His Ser Trp Asp Ala Leu Ile Lys
 275 280 285

His Ser Pro Arg Val Asn Val Val Met His Phe Phe Leu Tyr Glu Glu
 290 295 300

Glu Phe Glu Thr Phe Phe Lys Glu Glu Thr Pro Val Thr His Leu Tyr
 305 310 315 320

Phe Gly Arg Ser Val Ser Lys Val Val Leu Gly Arg Val Gly Leu Asn
 325 330 335

Cys Pro Arg Leu Ile Glu Leu Val Val Cys Ala Asn Asp Leu Gln Pro
 340 345 350

Leu Asp Asn Glu Leu Ile Cys Ile Ala Glu His Cys Thr Asn Leu Thr
 355 360 365

Ala Leu Gly Leu Ser Lys Cys Glu Val Ser Cys Ser Ala Phe Ile Arg
370 375 380

Phe Val Arg Leu Cys Glu Arg Arg Leu Thr Gln Leu Ser Val Met Glu
385 390 395 400

Glu Val Leu Ile Pro Asp Glu Asp Tyr Ser Leu Asp Glu Ile His Thr
405 410 415

Glu Val Ser Lys Tyr Leu Gly Arg Val Trp Phe Pro Asp Val Met Pro
420 425 430

Leu Trp

<210> 25
<211> 1970
<212> DNA
<213> Homo sapiens

<400> 25
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gcaaaaactgg cagttatccc tataatataa atttataatt tgattttta ttttaaaaac 1860
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<210> 26
<211> 634
<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> all Xaa positions

<223> Xaa=unknown amino acid residue

<400> 26

Glu Thr Ser Lys Leu Gly Ser Ala Val Leu Ala Pro Ala Ala Gly Gly
1 5 10 15

Thr Leu Ser Ser Glu Gly Arg Ser Ala Val Ser Gly Ile Leu Ile Ala
20 25 30

Val Thr Ser Thr Gly Val Asp Lys Ser Leu Asn Gln Leu Leu His Gly
35 40 45

Leu Gly Thr Ser Ser Arg Leu Ser His Phe Pro Phe Gly Lys Ser Pro
50 55 60

Pro Arg Gly Gln Phe Val Ala Ala Val Glu Ile Ala Gly Arg Ser
65 70 75 80

Gly Leu Gln Met Gly Gln Gly Leu Trp Arg Val Val Arg Asn Gln Gln
85 90 95

Leu Gln Gln Glu Gly Tyr Ser Glu Gln Gly Tyr Leu Thr Arg Glu Gln
100 105 110

Ser Arg Arg Met Ala Ala Ser Asn Ile Ser Asn Thr Asn His Arg Lys
115 120 125

Gln Val Gln Gly Gly Ile Asp Ile Tyr His Leu Leu Lys Ala Arg Lys
130 135 140

Ser Lys Glu Gln Glu Gly Phe Ile Asn Leu Glu Met Leu Pro Pro Glu
145 150 155 160

Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr Asp Leu Cys Leu
165 170 175

Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu Leu Leu Trp Gln
180 185 190

Gly Leu Cys Lys Ser Thr Trp Gly His Cys Ser Ile Tyr Asn Lys Asn
195 200 205

Pro Pro Leu Gly Phe Ser Phe Arg Lys Xaa Tyr Met Gln Leu Asp Glu
210 215 220

Gly Ser Leu Thr Phe Asn Ala Asn Pro Asp Glu Gly Val Asn Tyr Phe
225 230 235 240

Met Ser Lys Gly Ile Leu Asp Asp Ser Pro Lys Glu Ile Ala Lys Phe
245 250 255

Ile Phe Cys Thr Arg Thr Leu Asn Trp Lys Lys Leu Arg Ile Tyr Leu
260 265 270

Asp Glu Arg Arg Asp Val Leu Asp Asp Leu Val Thr Leu His Asn Phe

275

280

285

Arg Asn Gln Phe Leu Pro Asn Ala Leu Arg Glu Phe Phe Arg His Ile
 290 295 300
 His Ala Pro Glu Glu Arg Gly Glu Tyr Leu Glu Thr Leu Ile Thr Lys
 305 310 315 320
 Phe Ser His Arg Phe Cys Ala Cys Asn Pro Asp Leu Met Arg Glu Leu
 325 330 335
 Gly Leu Ser Pro Asp Ala Val Tyr Val Leu Cys Tyr Ser Leu Ile Leu
 340 345 350
 Leu Ser Ile Asp Leu Thr Ser Pro His Val Lys Asn Lys Met Ser Lys
 355 360 365
 Arg Glu Phe Ile Arg Asn Thr Arg Arg Ala Ala Gln Asn Ile Ser Glu
 370 375 380
 Asp Phe Val Gly His Leu Tyr Asp Asn Ile Tyr Leu Ile Gly His Val
 385 390 395 400
 Ala Ala Lys Ala Gln Leu Leu Gly Leu Gln Phe Leu Leu Gln Thr Lys
 405 410 415
 Ala Thr Gln Gly Leu Ser Arg Tyr Gly Gly Tyr Ile Ser Ala Gly His
 420 425 430
 Cys Ser Leu Ser Ile Gln Ser Ser Phe Ser Val Gln Pro Phe Phe Leu
 435 440 445
 Leu Pro Phe Ser Ile Leu Val Ile Ser Leu Gly Asn Ile Ile Leu Gln
 450 455 460
 Asn Phe Ser Phe Cys Leu Ser Arg Phe Ala Gln Ser Arg Ala Thr Val
 465 470 475 480
 His Ser Cys Arg Met Ile Asn His Tyr Thr Leu Lys Asp Gly Val Phe
 485 490 495
 Val His Ile Cys Leu Lys Asn Phe Ile His Phe His Ser Leu Tyr Lys
 500 505 510
 Tyr His Val Met Cys Thr Tyr Leu Thr Lys Glu Ile Tyr Ser His Asn
 515 520 525
 Tyr Phe Ile Val Lys Ile Leu Thr Lys Val Phe Pro Phe Leu Ser Asn
 530 535 540
 Val Leu Lys Phe Ile Phe Ser Glu Thr Ile Val Xaa Val Lys Val Arg
 545 550 555 560
 Ser Asp Phe Arg Gln Lys Pro Ile Pro Ala Ser Phe Ser Phe Lys Leu
 565 570 575
 Arg Val Leu Ile Cys Tyr Tyr Ile Thr Met Gln Asn Trp Gln Leu Phe
 580 585 590
 Leu Tyr Lys Phe Ile Ile Phe Phe Ile Leu Lys Thr Gly Leu Ile Lys
 595 600 605

Ser Arg Val Leu Thr Ile Asp Phe Asn Ile Lys Ile Tyr Asp Leu His
610 615 620

Ser Glu Asn Lys Ile Xaa Leu Glu Leu Trp
625 630

<210> 27
<211> 4168
<212> DNA
<213> Homo sapiens

<400> 27
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catcctgtgc tgcggctcgc tgacggccgc cgacatcgcc cgtgtctcca gcacctgccc 180
gcccgtgcgc gagctgtgcc agagcagccg gaaggtgtgg aaggagcgt tccgggttag 240
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taaagttcgg caaaaagctg ggttagaaagc gccgaagatt gtagcctcgt tctcaaagag 360
gttctttca gagcacgttc cttgtaatgg cttcagtgac attgagaacc ttgaaggacc 420
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taatcttaag gccttcttc agcagccaga tgactatgag tcgtatctg aaggtgttgt 600
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aattgacagc atcgtggagc ttgttgc aaacccttcgg ggcataaaca gtcgcccaccc 720
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cttggatat aacgtggagc ctcaagaaat ctcacaccct gacgtgggac getatttctc 1740
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tctacttcag tatcatgagt aggtcttaca tcagtgatgg gttcttttg tagtgagaca 2760
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<210> 28

<211> 621

<212> PRT

<213> Homo sapiens

<400> 28

Met Ala Ala Ala Ala Val Asp Ser Ala Met Glu Val Val Pro Ala Leu
1 5 10 15

Ala Glu Glu Ala Ala Pro Glu Val Ala Gly Leu Ser Cys Leu Val Asn
20 25 30

Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr
 35 40 45

Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu
50 55 60

Leu Cys Gln Ser Ser Gly Lys Val Trp Lys Glu Gln Phe Arg Val Arg
65 70 75 80

Trp Pro Ser Leu Met Lys His Tyr Ser Pro Thr Asp Tyr Val Asn Trp
85 90 95

Leu Glu Glu Tyr Lys Val Arg Gln Lys Ala Gly Leu Glu Ala Arg Lys
 100 105 110

Ile Val Ala Ser Phe Ser Lys Arg Phe Phe Ser Glu His Val Pro Cys
115 120 125

Asn	Gly	Phe	Ser	Asp	Ile	Glu	Asn	Leu	Glu	Gly	Pro	Glu	Ile	Phe	Phe
130					135							140			

Glu Asp Glu Leu Val Cys Ile Leu Asn Met Glu Gly Arg Lys Ala Leu
145 150 155 160

Thr Trp Lys Tyr Tyr Ala Lys Lys Ile Leu Tyr Tyr Leu Arg Gln Gln

165	170	175
Lys Ile Leu Asn Asn Leu Lys Ala Phe Leu Gln Gln Pro Asp Asp Tyr 180	185	190
Glu Ser Tyr Leu Glu Gly Ala Val Tyr Ile Asp Gln Tyr Cys Asn Pro 195	200	205
Leu Ser Asp Ile Ser Leu Lys Asp Ile Gln Ala Gln Ile Asp Ser Ile 210	215	220
Val Glu Leu Val Cys Lys Thr Leu Arg Gly Ile Asn Ser Arg His Pro 225	230	235
Ser Leu Ala Phe Lys Ala Gly Glu Ser Ser Met Ile Met Glu Ile Glu 245	250	255
Leu Gln Ser Gln Val Leu Asp Ala Met Asn Tyr Val Leu Tyr Asp Gln 260	265	270
Leu Lys Phe Lys Gly Asn Arg Met Asp Tyr Tyr Asn Ala Leu Asn Leu 275	280	285
Tyr Met His Gln Val Leu Ile Arg Arg Thr Gly Ile Pro Ile Ser Met 290	295	300
Ser Leu Leu Tyr Leu Thr Ile Ala Arg Gln Leu Gly Val Pro Leu Glu 305	310	315
Pro Val Asn Phe Pro Ser His Phe Leu Leu Arg Trp Cys Gln Gly Ala 325	330	335
Glu Gly Ala Thr Leu Asp Ile Phe Asp Tyr Ile Tyr Ile Asp Ala Phe 340	345	350
Gly Lys Gly Lys Gln Leu Thr Val Lys Glu Cys Glu Tyr Leu Ile Gly 355	360	365
Gln His Val Thr Ala Ala Leu Tyr Gly Val Val Asn Val Lys Lys Val 370	375	380
Leu Gln Arg Met Val Gly Asn Leu Leu Ser Leu Gly Lys Arg Glu Gly 385	390	395
Ile Asp Gln Ser Tyr Gln Leu Leu Arg Asp Ser Leu Asp Leu Tyr Leu 405	410	415
Ala Met Tyr Pro Asp Gln Val Gln Leu Leu Leu Leu Gln Ala Arg Leu 420	425	430
Tyr Phe His Leu Gly Ile Trp Pro Glu Lys Val Leu Asp Ile Leu Gln 435	440	445
His Ile Gln Thr Leu Asp Pro Gly Gln His Gly Ala Val Gly Tyr Leu 450	455	460
Val Gln His Thr Leu Glu His Ile Glu Arg Lys Lys Glu Glu Val Gly 465	470	475
Val Glu Val Lys Leu Arg Ser Asp Glu Lys His Arg Asp Val Cys Tyr		

485

490

495

Ser Ile Gly Leu Ile Met Lys His Lys Arg Tyr Gly Tyr Asn Cys Val
500 505 510

Ile Tyr Gly Trp Asp Pro Thr Cys Met Met Gly His Glu Trp Ile Arg
515 520 525

Asn Met Asn Val His Ser Leu Pro His Gly His His Gln Pro Phe Tyr
530 535 540

Asn Val Leu Val Glu Asp Gly Ser Cys Arg Tyr Ala Ala Gln Glu Asn
545 550 555 560

Leu Glu Tyr Asn Val Glu Pro Gln Glu Ile Ser His Pro Asp Val Gly
565 570 575

Arg Tyr Phe Ser Glu Phe Thr Gly Thr His Tyr Ile Pro Asn Ala Glu
580 585 590

Leu Glu Ile Arg Tyr Pro Glu Asp Leu Glu Phe Val Tyr Glu Thr Val
595 600 605

Gln Asn Ile Tyr Ser Ala Lys Lys Glu Asn Ile Asp Glu
610 615 620

<210> 29

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> all n positions

<223> n=a, c, g or t

<400> 29

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tccccgggntc ctccgtagac ccgcgganac cttcgtgttg agtaacctgg cggaggtgg 120
ggagcgtgtg ctcacccccc tgccccccaa ggcgttgctg cgggtggcct gcgtgtgccg 180
cttatggagg gagtgtgtgc gcagagtatt gcgacccat cggagcgtaa cctggatctc 240
cgcaggcctg gcggaggccg gccacctggn gggcatt 278

<210> 30

<211> 91

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> all Xaa positions

<223> Xaa=unknown amino acid residue

<400> 30

Arg Ser Thr Gly Phe Arg Arg Ala Gly Glu Glu Trp Ser Arg Xaa Leu
1 5 10 15

Ala Ala Ser Pro Gly Xaa Leu Arg Arg Pro Ala Xaa Thr Phe Val Leu
20 25 30

Ser Asn Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala
35 40 45

Lys Ala Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys
50 55 60

Val Arg Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile Ser Ala
65 70 75 80

Gly Leu Ala Glu Ala Gly His Leu Xaa Gly His
85 90

<210> 31

<211> 592

<212> DNA

<213> Homo sapiens

<400> 31

gcggccgcgc ccgtgcagc aacagcagca gcagcccccg cagcagccgc cgccgcagcc 60
gccccagcag cagccgcccc agcagcagcc tccgcgcgc cgcgcagcagc agcagcagca 120
gcagcctccg cgcgcgcac cgccgcctcc gcccgtgcct caggagcggaa acaacgtcgg 180
cgagcggat gatgtatgtc ctgcagatata gttgcagaa gaatcaggta ctgggtgcaca 240
aaatagtcca taccaacttc gttagaaaaac tctttgccg aaaagaacag cgtgtcccac 300
aaagaacagt atggaggcgc cctcaacttc aactacagaa aacttggtc atcgtgcaaa 360
acgtgcaaga gtgtctggaa aatcacaaga tctatcagca gcacctgctg aacagtatct 420
tcaggagaaa ctgcagatg aagtggttct aaaaatcttc tcttacttgc tggaacagga 480
tctttgtaga gcagcttgc tatgtaaacg ctgcgtgaa ctgcataatg atcccaattt 540
gtggaaacgaa ttatatatgg aagtatttga atatactcgc cctatgatgc at 592

<210> 32

<211> 197

<212> PRT

<213> Homo sapiens

<400> 32

Arg Pro Arg Pro Val Gln Gln Gln Gln Gln Pro Pro Gln Gln Pro
1 5 10 15

Pro Pro Gln Pro Pro Gln Gln Gln Pro Pro Gln Gln Pro Pro Pro
20 25 30

Pro Pro Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro
35 40 45

Pro Pro Pro Leu Pro Gln Glu Arg Asn Asn Val Gly Glu Arg Asp Asp
50 55 60

Asp Val Pro Ala Asp Met Val Ala Glu Glu Ser Gly Pro Gly Ala Gln
65 70 75 80

Asn Ser Pro Tyr Gln Leu Arg Arg Lys Thr Leu Leu Pro Lys Arg Thr
85 90 95

Ala Cys Pro Thr Lys Asn Ser Met Glu Gly Ala Ser Thr Ser Thr Thr
100 105 110

Glu Asn Phe Gly His Arg Ala Lys Arg Ala Arg Val Ser Gly Lys Ser
115 120 125

Gln Asp Leu Ser Ala Ala Pro Ala Glu Gln Tyr Leu Gln Glu Lys Leu

130	135	140
Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln Asp		
145	150	155
Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala Asn		
165	170	175
Asp Pro Asn Leu Trp Lys Arg Leu Tyr Met Glu Val Phe Glu Tyr Thr		
180	185	190
Arg Pro Met Met His		
195		

<210> 33
<211> 537
<212> DNA
<213> Homo sapiens

<400> 33

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gccccccgcgg cccggactcc gcggtggcg agcgccctgt gaggtgacca tggaggctgg 60
tggcctcccc ttggagctgt ggcgcatgtat cttagcctac ttgcacccctc ccgcacctggg 120
ccgctgcagc ctggtatgca gggcctggta tgaactgatc ctcagtcgtc acagcacccg 180
ctggcggcag ctgtgtctgg gttgcaccga gtgccgcccatt cccaattggc ccaaccagcc 240
agatgtggag cctgagtc ttggagagaagc cttaaaggcag cattacccat catccaagac 300
atggaccaag aatgccttgg acttggagtc ttccatctgc tttctctat tccgcccggag 360
gagggAACGA cgtaccctga gtgttggcc agggcgtgag tttgacagcc tgggcagtgc 420
cttggccatg gccagcctgt atgaccgaat tgtctcttc ccaggtgtgt acgaagagca 480
agtgaaatc atcttgaagg tgcctgtgga gattgttaggg cagggaaatc tgggtga 537
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<210> 34
<211> 178
<212> PRT
<213> Homo sapiens

<400> 34

Arg Pro Arg Pro Gly Leu Arg Gly Gly Arg Ala Pro Cys Glu Val Thr			
1	5	10	15
Met Glu Ala Gly Gly Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala			
20	25	30	

Tyr Leu His Leu Pro Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala			
35	40	45	

Trp Tyr Glu Leu Ile Leu Ser Leu Asp Ser Thr Arg Trp Arg Gln Leu			
50	55	60	

Cys Leu Gly Cys Thr Glu Cys Arg His Pro Asn Trp Pro Asn Gln Pro			
65	70	75	80

Asp Val Glu Pro Glu Ser Trp Arg Glu Ala Phe Lys Gln His Tyr Leu			
85	90	95	

Ala Ser Lys Thr Trp Thr Lys Asn Ala Leu Asp Leu Glu Ser Ser Ile			
100	105	110	

Cys Phe Ser Leu Phe Arg Arg Arg Glu Arg Arg Thr Leu Ser Val			
115	120	125	

Gly Pro Gly Arg Glu Phe Asp Ser Leu Gly Ser Ala Leu Ala Met Ala
130 135 140

Ser Leu Tyr Asp Arg Ile Val Leu Phe Pro Gly Val Tyr Glu Glu Gln
145 150 155 160

Gly Glu Ile Ile Leu Lys Val Pro Val Glu Ile Val Gly Gln Gly Lys
165 170 175

Leu Gly

<210> 35

<211> 751

<212> DNA

<213> Homo sapiens

<400> 35

gagaccgaga cggcgccgct gaccctagag tcgctgccca ccgatcccct gctcctcatc 60
ttatcctttt tggactatcg gnatctaatac aactgttgtt atgtcagtgc aagattaagc 120
cagctatcaa gtcatgatcc gctgtggaga agacattgca aaaaataactg gctgatatact 180
gaggaagaga aaacacagaa gaatcagtgt tggaaatctc tcttcataaga tacttactct 240
gatgttagaa gatacattga ccattatgct gctattaaaa aggccctcggg aatgatctca 300
agaaatattt ggagcccagg tgtcctcgga tggttttat ctctgaaaga ggggtgctcg 360
agaggaagac ctcgatgctg tggaagcgca gattgggctg caagtttcct ggacgattat 420
cgatgttcat accgaattca caatggacag aagtttagttt gttcctgggg ttattggaa 480
gcatggcact gtctaattcac tatcgttctg aagatttgtt agacgtcgt acagctgccc 540
gagattccag cagagacagg gactgaaata ctgtctccct ttaactttt catacatact 600
ggttgagtc agtacatagc agtggaaagct gcagagggtt gaaacaaaaa tgaagtttc 660
taccaatgtc agacagtaga acgtgtgtt aaatatggca ttaagatgtg ttctgatgg 720
tgtataaatg gcatgcatta ggtattttca g 751

<210> 36

<211> 247

<212> PRT

<213> Homo sapiens

<400> 36

Glu Thr Glu Thr Ala Pro Leu Thr Leu Glu Ser Leu Pro Thr Asp Pro
1 5 10 15

Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg Asp Leu Ile Asn Cys
20 25 30

Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser Ser His Asp Pro Leu
35 40 45

Trp Arg Arg His Cys Lys Lys Tyr Trp Leu Ile Ser Glu Glu Lys
50 55 60

Thr Gln Lys Asn Gln Cys Trp Lys Ser Leu Phe Ile Asp Thr Tyr Ser
65 70 75 80

Asp Val Gly Arg Tyr Ile Asp His Tyr Ala Ala Ile Lys Lys Ala Ser
85 90 95

Gly Met Ile Ser Arg Asn Ile Trp Ser Pro Gly Val Leu Gly Trp Val
100 105 110

Leu Ser Leu Lys Glu Gly Cys Ser Arg Gly Arg Pro Arg Cys Cys Gly

115	120	125	
Ser Ala Asp Trp Ala Ala Ser Phe Leu Asp Asp Tyr Arg Cys Ser Tyr			
130	135	140	
Arg Ile His Asn Gly Gln Lys Leu Val Gly Ser Trp Gly Tyr Trp Glu			
145	150	155	160
Ala Trp His Cys Leu Ile Thr Ile Val Leu Lys Ile Cys Thr Ser Ile			
165	170	175	
Gln Leu Pro Glu Ile Pro Ala Glu Thr Gly Thr Glu Ile Leu Ser Pro			
180	185	190	
Phe Asn Phe Cys Ile His Thr Gly Leu Ser Gln Tyr Ile Ala Val Glu			
195	200	205	
Ala Ala Glu Gly Asn Lys Asn Glu Val Phe Tyr Gln Cys Gln Thr Val			
210	215	220	
Glu Arg Val Phe Lys Tyr Gly Ile Lys Met Cys Ser Asp Gly Cys Ile			
225	230	235	240
Asn Gly Met His Val Phe Ser			
245			

<210> 37
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 37
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caggaacctg aggtcggctg ctgcggaaa tacttcctgt ttggcttcaa cattgtcttc 120
tgggtgctgg gagccctgtt cctggctatac gcgcctctggg cctgggggtga gaagggcggtt 180
ctctcgaaca tctcagcgct gacagatctg ggaggccttg accccgtgtg gcttgtttgt 240
ggtagttgga ggcgtcatgt cggtgctggg ctttgctggg ctgcaattgg ggccctccgg 300
gagaacacct tcctgctcaa gttttctnc gnnttcctcg gtctcatctt cttcctggag 360
ctggcaac 368

<210> 38
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

<400> 38
Gly Ser Gly Phe Arg Ala Gly Gly Trp Pro Leu Thr Met Pro Gly Lys
1 5 10 15

His Gln His Phe Gln Glu Pro Glu Val Gly Cys Cys Gly Lys Tyr Phe

20

25

30

Leu Phe Gly Phe Asn Ile Val Phe Trp Val Leu Gly Ala Leu Phe Leu
 35 40 45

Ala Ile Gly Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile
 50 55 60

Ser Ala Leu Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys
 65 70 75 80

Gly Ser Trp Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala Ala Ile
 85 90 95

Gly Ala Leu Arg Glu Asn Thr Phe Leu Leu Lys Phe Phe Xaa Xaa Phe
 100 105 110

Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala
 115 120

<210> 39

<211> 774

<212> DNA

<213> Homo sapiens

<400> 39

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 gagctggtgg acggccccc gctgtggctg ctcaagtgcc agcaggaggg gctgggtgccc 180
 gagggcggcg tggaggagga ggcgcaccac tggcagcagt tctacttcct gagcaagcgg 240
 cggcgcacc ttctgcgtaa cccgtgtggg gaagaggact tggaaaggctg gtgtgacgtg 300
 gagcatggtg gggacggctg gagggtggag gagctgcctg gagacagtgg gttggagttc 360
 acccacatgc agagcgtcaa gaagtacttc gcctcctcct ttgagttgtg tcgcaaagca 420
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 gccatcgtgg tgaaggactg gtactcgggc cgcagcgcacg ctgggtgcct ctacgagctc 540
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 gcagtgcacc aagacagtga cggcggggc tggatggaga tctcccacac cttcaccgac 660
 tacgggcccgg gcgtccgctt cgtccgcttc gagcacgggg ggcagggtc cgtctactgg 720
 aagggtgtt tcggggcccg ggtgaccaac agcagcgtgt ggtagaaacc ctga 774

<210> 40

<211> 257

<212> PRT

<213> Homo sapiens

<400> 40

Ala Ala Ala Ala Ala Ala Tyr Leu Asp Glu Leu Pro Glu Pro Leu Leu
 1 5 10 15

Leu Arg Val Leu Ala Ala Leu Pro Ala Ala Glu Leu Val Gln Ala Cys
 20 25 30

Arg Leu Val Cys Leu Arg Trp Lys Glu Leu Val Asp Gly Ala Pro Leu
 35 40 45

Trp Leu Leu Lys Cys Gln Gln Glu Gly Leu Val Pro Glu Gly Gly Val
 50 55 60

Glu Glu Glu Arg Asp His Trp Gln Gln Phe Tyr Phe Leu Ser Lys Arg
 65 70 75 80

Arg Arg Asn Leu Leu Arg Asn Pro Cys Gly Glu Glu Asp Leu Glu Gly
 85 90 95

 Trp Cys Asp Val Glu His Gly Gly Asp Gly Trp Arg Val Glu Glu Leu
 100 105 110

 Pro Gly Asp Ser Gly Val Glu Phe Thr His Asp Glu Ser Val Lys Lys
 115 120 125

 Tyr Phe Ala Ser Ser Phe Glu Trp Cys Arg Lys Ala Gln Val Ile Asp
 130 135 140

 Leu Gln Ala Glu Gly Tyr Trp Glu Glu Leu Leu Asp Thr Thr Gln Pro
 145 150 155 160

 Ala Ile Val Val Lys Asp Trp Tyr Ser Gly Arg Ser Asp Ala Gly Cys
 165 170 175

 Leu Tyr Glu Leu Thr Val Lys Leu Leu Ser Glu His Glu Asn Val Leu
 180 185 190

 Ala Glu Phe Ser Ser Gly Gln Val Ala Val Pro Gln Asp Ser Asp Gly
 195 200 205

 Gly Gly Trp Met Glu Ile Ser His Thr Phe Thr Asp Tyr Gly Pro Gly
 210 215 220

 Val Arg Phe Val Arg Phe Glu His Gly Gln Gly Ser Val Tyr Trp
 225 230 235 240

 Lys Gly Trp Phe Gly Ala Arg Val Thr Asn Ser Ser Val Trp Val Glu
 245 250 255

Pro

<210> 41
 <211> 957
 <212> DNA
 <213> Homo sapiens

<400> 41
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 cgcacatgttc gcagactcag tccgcgcctc caagatcagg acacgaagg cctgtatttc 300
 caggcatttg gagggccgccc ccgatgtctc agcaagagcg tggccccctt gctagcccac 360
 ggctaccgccc gcttcttgcc caccaaggat cacgttctca ttcttgacta cgtggggacc 420
 ctcttcttccc tcaaaaatgc cctggtctcc accctcgccc agatgcagtgcg gaagcgggccc 480
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<210> 42
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 42
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Ser Cys Pro Ser Cys Gly Ser Glu Leu Gly Val Glu Glu Lys Arg Gly
 20 25 30

Lys Gly Asn Pro Ile Ser Ile Gln Leu Phe Pro Pro Glu Leu Val Glu
 35 40 45

His Ile Ile Ser Phe Leu Pro Val Arg Asp Leu Val Ala Leu Gly Gln
 50 55 60

Thr Cys Arg Tyr Phe His Glu Val Cys Asp Gly Glu Gly Val Trp Arg
 65 70 75 80

Arg Ile Cys Arg Arg Leu Ser Pro Arg Leu Gln Asp Gln Asp Thr Lys
 85 90 95

Gly Leu Tyr Phe Gln Ala Phe Gly Gly Arg Arg Arg Cys Leu Ser Lys
 100 105 110

Ser Val Ala Pro Leu Leu Ala His Gly Tyr Arg Arg Phe Leu Pro Thr
 115 120 125

Lys Asp His Val Phe Ile Leu Asp Tyr Val Gly Thr Leu Phe Phe Leu
 130 135 140

Lys Asn Ala Leu Val Ser Thr Leu Gly Gln Met Gln Trp Lys Arg Ala
 145 150 155 160

Cys Arg Tyr Val Val Leu Cys Arg Gly Ala Lys Asp Phe Ala Ser Asp
 165 170 175

Pro Arg Cys Asp Thr Val Tyr Arg Lys Tyr Leu Tyr Val Leu Ala Thr
 180 185 190

Arg Glu Pro Gln Glu Val Val Gly Thr Thr Ser Ser Arg Ala Cys Asp
 195 200 205

Cys Val Glu Val Tyr Leu Gln Ser Ser Gly Gln Arg Val Phe Lys Met
 210 215 220

Thr Phe His His Ser Met Thr Phe Lys Gln Ile Val Leu Val Gly Gln
 225 230 235 240

Glu Thr Gln Arg Ala Leu Leu Leu Thr Glu Glu Gly Lys Ile Tyr
 245 250 255

Ser Leu Val Val Asn Glu Thr Gln Leu Asp Gln Pro Arg Ser Tyr Thr
 260 265 270

Val Gln Leu Ala Leu Arg Lys Val Ser His Tyr Leu Pro His Leu Arg
 275 280 285

Val Ala Cys Met Thr Ser Asn Gln Ser Ser Thr Leu Tyr Val Thr Asp
290 295 300

Pro Ile Leu Cys Ser Trp Leu Gln Pro Pro Trp Pro Gly Gly
305 310 315

<210> 43

<211> 1590

<212> DNA

<213> Homo sapiens

<400> 43

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ggggctgagg cgggagcgag gacacgcca agagaggaag cagagggagg cgaaagcgtg 180
gaggaagggg cgagaggcat catcaaagga gatgagggga gcttagggc cgggaaagag 240
gcacaaggaa gaaagtatgg gaaggaggaa tggagggtca gggcttaggcg gccccgggc 300
gcacaggccg gaagagtaca aggacaagga ggtcagggtt gggcctacat cccggggaca 360
ggggcggcca tggcggccg acccaggag gaggaggagg aggcggctcg ggagtcaagcc 420
gcctgcccgg ctgcggggcc acgcgtctgg cgccctggcc aagtgtcgat gtcacatg 480
tgctccatcc tcgacatgca ggcctctggc cgccctggccc aggtgtaccg ctggctgtgg 540
cacttcacca actgcgaccc gctccggcgc cagatagcc gggcctcgat caactccggc 600
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ctccacgtcc tggatattca aaaccctgtga 1590

<210> 44

<211> 529

<212> PRT

<213> Homo sapiens

<400> 44

Arg Gly Gly Ser Glu Gly Arg Gly Arg Gly Arg Glu Lys Arg Ala Arg
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Gly Ala Arg Arg Lys Arg Lys Gln Gly Gly Arg Glu Ala Arg Ala Ala
20 25 30

Asp Gly Glu Gly Gly Ser Gly Pro Gly Ala Glu Ala Gly Ala Arg Thr
35 40 45

Arg Pro Arg Glu Glu Ala Glu Gly Gly Ser Val Glu Glu Gly Ala
50 55 60

Arg Gly Ile Ile Lys Gly Asp Glu Gly Ser Val Gly Ala Gly Lys Glu
65 70 75 80

Ala Gln Gly Arg Lys Tyr Gly Lys Glu Glu Trp Arg Val Arg Ala Arg
 85 90 95

 Arg Arg Glu Gly Ala Arg Pro Gly Arg Val Gln Gly Gln Gly Gln
 100 105 110

 Val Trp Ala Tyr Ile Pro Gly Thr Gly Ala Ala Met Ala Ala Ala Ala
 115 120 125

 Arg Glu Glu Glu Glu Ala Ala Arg Glu Ser Ala Ala Cys Pro Ala
 130 135 140

 Ala Gly Pro Ala Leu Trp Arg Leu Pro Glu Val Leu Leu Leu His Met
 145 150 155 160

 Cys Ser Tyr Leu Asp Met Arg Ala Leu Gly Arg Leu Ala Gln Val Tyr
 165 170 175

 Arg Trp Leu Trp His Phe Thr Asn Cys Asp Leu Leu Arg Arg Gln Ile
 180 185 190

 Ala Trp Ala Ser Leu Asn Ser Gly Phe Thr Arg Leu Gly Thr Asn Leu
 195 200 205

 Met Thr Ser Val Pro Val Lys Val Ser Gln Asn Trp Ile Val Gly Cys
 210 215 220

 Cys Arg Glu Gly Ile Leu Lys Trp Arg Cys Ser Gln Met Pro Trp
 225 230 235 240

 Met Gln Leu Glu Asp Asp Ala Leu Tyr Ile Ser Gln Ala Asn Phe Ile
 245 250 255

 Leu Ala Tyr Gln Phe Arg Pro Asp Gly Ala Ser Leu Asn Arg Gln Pro
 260 265 270

 Leu Gly Val Ser Ala Gly His Asp Glu Asp Val Cys His Phe Val Leu
 275 280 285

 Ala Thr Ser His Ile Val Ser Ala Gly Gly Asp Gly Lys Ile Gly Leu
 290 295 300

 Gly Lys Ile His Ser Thr Phe Ala Ala Lys Tyr Trp Ala His Glu Gln
 305 310 315 320

 Glu Val Asn Cys Val Asp Cys Lys Gly Gly Ile Ile Ser Phe Gly Ser
 325 330 335

 Arg Asp Arg Thr Ala Lys Val Trp Pro Leu Ala Ser Gly Gln Leu Gly
 340 345 350

 Gln Cys Leu Tyr Thr Ile Gln Thr Glu Asp Gln Ile Trp Ser Val Ala
 355 360 365

 Ile Arg Pro Leu Leu Ser Ser Phe Val Thr Gly Thr Ala Cys Cys Gly
 370 375 380

 His Phe Ser Pro Leu Lys Ile Trp Asp Leu Asn Ser Gly Gln Leu Met
 385 390 395 400

Thr His Leu Asp Arg Asp Phe Pro Pro Arg Ala Gly Val Leu Asp Val
 405 410 415

 Ile Tyr Glu Ser Pro Phe Ala Leu Leu Ser Cys Gly Tyr Asp Thr Tyr
 420 425 430

 Val Arg Tyr Trp Asp Cys Arg Thr Ser Val Arg Lys Cys Val Met Glu
 435 440 445

 Trp Glu Glu Pro His Asn Ser Thr Leu Tyr Cys Leu Gln Thr Asp Gly
 450 455 460

 Asn His Leu Leu Ala Thr Gly Ser Ser Phe Tyr Ser Val Val Arg Leu
 465 470 475 480

 Trp Asp Arg His Gln Arg Ala Cys Pro His Thr Phe Pro Leu Thr Ser
 485 490 495

 Thr Arg Leu Gly Ser Pro Val Tyr Cys Leu His Leu Thr Thr Lys His
 500 505 510

 Leu Tyr Ala Ala Leu Ser Tyr Asn Leu His Val Leu Asp Ile Gln Asn
 515 520 525

 Pro

<210> 45
 <211> 1214
 <212> DNA
 <213> Homo sapiens

<400> 45
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 tcttttggc taatttacta attttaactt ctgtgttgct tttccagagg catggctatt 180
 gcaccttggg agaaggcctt aatcggttag acttctcaag tgcaattcaa gatatccgaa 240
 cgttcaatta tgtggtcaaa ctgttgacg taattgcaaa atcccagtta acttcattga 300
 gtggcgtggc acagaagaat tacttcaaca ttttggataa aatcgttcaa aagggttcttg 360
 atgaccacca caatcctcgc ttaatcaaag atcttctgca agacctaagc tctaccctct 420
 gcattcttat tagaggagta gggaaagtctg tattagtggg aaacatcaat atttggattt 480
 gccgattaga aactattctc gcctggcaac aacagctaca ggatcttcag atgactaagc 540
 aagtgaacaa tggccctcacc ctcagtgacc ttccctctgca catgctgaac aacatcctat 600
 acccggtctc agacggatgg gacatcatca ccttaggcca ggtgaccccc acgttgtata 660
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 agttttgttag acatttgate ctttcagaaa aaggtcatat tgaatggaag ttgatgtact 780
 ttgcacttca gaaacattac ccagcgaagg agcagttacgg agacacactg catttctgtc 840
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 aactgccctt ctgcaaagggg gggactgcat ggttgcattt tcataactga aagtcaagg 1140

ccaaggaaaat catttctact tctttaaaaa ctccttctaa gcataattaaa atgtgaaatt 1200
 ttgcgtactc tctc 1214

<210> 46
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 46
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 Leu Gly Glu Ala Phe Asn Arg Leu Asp Phe Ser Ser Ala Ile Gln Asp
 20 25 30

 Ile Arg Thr Phe Asn Tyr Val Val Lys Leu Leu Gln Leu Ile Ala Lys
 35 40 45

 Ser Gln Leu Thr Ser Leu Ser Gly Val Ala Gln Lys Asn Tyr Phe Asn
 50 55 60

 Ile Leu Asp Lys Ile Val Gln Lys Val Leu Asp Asp His His Asn Pro
 65 70 75 80

 Arg Leu Ile Lys Asp Leu Leu Gln Asp Leu Ser Ser Thr Leu Cys Ile
 85 90 95

 Leu Ile Arg Gly Val Gly Lys Ser Val Leu Val Gly Asn Ile Asn Ile
 100 105 110

 Trp Ile Cys Arg Leu Glu Thr Ile Leu Ala Trp Gln Gln Gln Leu Gln
 115 120 125

 Asp Leu Gln Met Thr Lys Gln Val Asn Asn Gly Leu Thr Leu Ser Asp
 130 135 140

 Leu Pro Leu His Met Leu Asn Asn Ile Leu Tyr Arg Phe Ser Asp Gly
 145 150 155 160

 Trp Asp Ile Ile Thr Leu Gly Gln Val Thr Pro Thr Leu Tyr Met Leu
 165 170 175

 Ser Glu Asp Arg Gln Leu Trp Lys Lys Leu Cys Gln Tyr His Phe Ala
 180 185 190

 Glu Lys Gln Phe Cys Arg His Leu Ile Leu Ser Glu Lys Gly His Ile
 195 200 205

 Glu Trp Lys Leu Met Tyr Phe Ala Leu Gln Lys His Tyr Pro Ala Lys
 210 215 220

 Glu Gln Tyr Gly Asp Thr Leu His Phe Cys Arg His Cys Ser Ile Leu
 225 230 235 240

 Phe Trp Lys Asp Ser Gly His Pro Cys Thr Ala Ala Asp Pro Asp Ser
 245 250 255

 Cys Phe Thr Pro Val Ser Pro Gln His Phe Ile Asp Leu Phe Lys Phe
 260 265 270

<210> 47
 <211> 4059
 <212> DNA

<213> Homo sapiens

<400> 47

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atttatctgt	tttaaaaacat	tgcttccttc	ctggctctgc	taaattgaat	gctcattgtt	3960
tgttgtgtt	gttttttaat	tctaatgttc	aaatcaactgc	gtgctgtatg	aatctagaaa	4020
gccttaattt	actaccaaga	aataaagcaa	tatgttctgt			4059

<210> 48
<211> 483
<212> PRT
<213> *Homo sapiens*

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<400> 48
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      1           5           10          15

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Ser Ser Thr Asp His Thr Pro Thr Lys Ala Gln Lys Asn Val Ala Thr
20 25 30

Ser Glu Asp Ser Asp Leu Ser Met Arg Thr Leu Ser Thr Pro Ser Pro
35 40 45

Ala Leu Ile Cys Pro Pro Asn Leu Pro Gly Phe Gln Asn Gly Arg Gly
50 55 60

Ser Ser Thr Ser Ser Ser Ile Thr Gly Glu Thr Val Ala Met Val
65 70 75 80

His Ser Pro Pro Pro Thr Arg Leu Thr His Pro Leu Ile Arg Leu Ala
85 90 95

Ser Arg Pro Gln Lys Glu Gln Ala Ser Ile Asp Arg Leu Pro Asp His
100 105 110

Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn Gln Leu Cys Arg
115 120 125

Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala Trp Asp Pro Arg
130 135 140

Leu Trp Arg Thr Ile Arg Leu Thr Gly Glu Thr Ile Asn Val Asp Arg
145 150 155 160

Ala Leu Lys Val Leu Thr Arg Arg Leu Cys Gln Asp Thr Pro Asn Val
165 170 175

Asp Arg Gly Leu Tyr Thr Ile Ala Gln Cys Cys Pro Glu Leu Arg Arg
195 200 205

Leu Glu Val Ser Gly Cys Tyr Asn Ile Ser Asn Glu Ala Val Phe Asp
210 215 220

Val Val Ser Leu Cys Pro Asn Leu Glu His Leu Asp Val Ser Gly Cys
 225 230 235 240
 Ser Lys Val Thr Cys Ile Ser Leu Thr Arg Glu Ala Ser Ile Lys Leu
 245 250 255
 Ser Pro Leu His Gly Lys Gln Ile Ser Ile Arg Tyr Leu Asp Met Thr
 260 265 270
 Asp Cys Phe Val Leu Glu Asp Glu Gly Leu His Thr Ile Ala Ala His
 275 280 285
 Cys Thr Gln Leu Thr His Leu Tyr Leu Arg Arg Cys Val Arg Leu Thr
 290 295 300
 Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu
 305 310 315 320
 Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu
 325 330 335
 Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
 340 345 350
 Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
 355 360 365
 Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
 370 375 380
 Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
 385 390 395 400
 Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
 405 410 415
 Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
 420 425 430
 Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
 435 440 445
 Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
 450 455 460
 Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
 465 470 475 480
 Ala Phe Phe

<210> 49
 <211> 850
 <212> DNA
 <213> Homo sapiens

<400> 49
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 ggcggacggc cccatgcctt tcctggcag ggctgcgcgc gtgtgcgcgc gctggcaggaa 180

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gcccatacg	tttccacagc	tccagaggct	gaccctcatc	cactggaaat	ctcaggta	360
ccccgtgtt	aagctggtag	gtgagtgtcg	tcctcggtc	actttctca	agctctccgg	420
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gggcgcattt	ctgggcagct	gctgccccca	gctccaggtc	ctggaggtga	gcaccggcat	660
caaccgtaat	agcattcccc	ttcagctgcc	tgtcgaggct	ctgcagaaaag	gctgcctca	720
gctccagggt	ctgcggctgt	tgaacctgat	gtggctgccc	aaggctccgg	gacgagggggt	780
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ctttgtgagc						850

<210> 50
<211> 283
<212> PRT
<213> *Homo sapiens*

<400> 50
Ala Ala Ala Pro Ala Pro Ala Pro Ala Pro Thr Pro Thr Pro Glu Glu
1 5 10 15

Gly Pro Asp Ala Gly Trp Gly Asp Arg Ile Pro Leu Glu Ile Leu Val
20 25 30

Gln Ile Phe Gly Leu Leu Val Ala Ala Asp Gly Pro Met Pro Phe Leu
 35 40 45

Gly Arg Ala Ala Arg Val Cys Arg Arg Trp Gln Glu Ala Ala Ser Gln
50 55 60

Pro Ala Leu Trp His Thr Val Thr Leu Ser Ser Pro Leu Val Gly Arg
65 70 75 80

Pro Ala Lys Gly Gly Val Lys Ala Glu Lys Lys Leu Leu Ala Ser Leu
85 90 95

Glu Trp Leu Met Pro Asn Arg Phe Ser Gln Leu Gln Arg Leu Thr Leu
 100 105 110

Ile His Trp Lys Ser Gln Val His Pro Val Leu Lys Leu Val Gly Glu
 115 120 125

Cys Cys Pro Arg Leu Thr Phe Leu Lys Leu Ser Gly Cys His Gly Val
130 135 140

Thr Ala Asp Ala Leu Val Met Leu Ala Lys Ala Cys Cys Gln Leu His
145 150 155 160

Ser Leu Asp Leu Gln His Ser Met Val Glu Ser Thr Ala Val Val Ser
165 170 175

Phe Leu Glu Glu Ala Gly Ser Arg Met Arg Lys Leu Trp Leu Thr Tyr
 180 185 190

Ser Ser Gln Thr Thr Ala Ile Leu Gly Ala Leu Leu Gly Ser Cys Cys
195 200 205

Pro Gin Leu Gln Val Leu Glu Val Ser Thr Gly Ile Asn Arg Asn Ser
210 215 220

Ile Pro Leu Gln Leu Pro Val Glu Ala Leu Gln Lys Gly Cys Pro Gln
 225 230 235 240

Leu Gln Val Leu Arg Leu Leu Asn Leu Met Trp Leu Pro Lys Pro Pro
245 250 255

Gly Arg Gly Val Ala Pro Gly Pro Gly Phe Pro Ser Leu Glu Glu Leu
 260 265 270

Cys Leu Ala Ser Ser Thr Cys Asn Phe Val Ser
275 280

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<210> 51  
<211> 1777  
<212> DNA  
<213> Homo sapiens
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<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t
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<400> 51
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agaagtgtca gaacactcca caggataac ccatttcct cctgaggta tgctgtcaat 180
tttcagctat cttaatcctc aagagttatg tcgatgcagt caagtaagca taaaaatggc 240
tcagctgaca aaaacgggat cgcttggaa acatcttac cctgttcatt gggccagagg 300
tgactggtat agtggtcccg caactgaact tgatactgaa cctgatgatg aatgggtgaa 360
aaatagggaaa gatgaaagtc gtgctttca tgagtggtt gaaatgctg acattgtatg 420
atctgaagag tctgcggagg aatcaattgc tattcagcatt gcacaaatgg aaaaacgttt 480
actccatggc ttaattcata acgttctacc atatgttggt acttctgtaa aaaccttagt 540
attagcatac agctctgcag tttccagcaa aatgggttagg cagattttag agctttgtcc 600
taacctggag catctggatc ttaccagac tgacattca gattctgcat ttgacagttg 660
gtcttggctt ggttgcgtcc agagtttcg gcatcttgat ctgtctgggtt gtgagaaaaat 720
cacagatgtg gcccttagaga agatttccag agctcttggaa attctgacat ctcatcaaag 780
tggcttttg aaaacatcta caagaaaaat tacttcaact gcgtggaaaa ataaagacat 840
taccatgcag tccacccaagc agtatgcctg tttgcacat ttaactaaca agggcattgg 900
agaagaaaata gataatgaac accccctggac taagcctgtt tcttctgaga atttcacttc 960
tccttatgtg tggatgttag atgctgaaga tttggctgtt attgaagata ctgtggaatg 1020
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cagggttttgc actctggag gagggctgcc ttatggag cacccttaatc tctctgggtt 1440
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catttcttgc gttaccatc cttttttgag cgtgacttgc tttggggccca ttynyttacaa 1740
cttcqaatggaaaat cttaatattacc aqgtgrattgt aatgttttgc 1777

<210> 52
<211> 590
<212> PRT
<213> *Homo sapiens*

<220>
 <221> SITE
 <222> all Xaa positions
 <223> Xaa=unknown amino acid residue

<400> 52
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 1 5 10 15

Leu Trp Asn His Ala Glu Glu Arg Gln Lys Phe Phe Lys Tyr Ser Val
 20 25 30

Asp Glu Lys Ser Asp Lys Glu Ala Glu Val Ser Glu His Ser Thr Gly
 35 40 45

Ile Thr His Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu
 50 55 60

Asn Pro Gln Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser
 65 70 75 80

Gln Leu Thr Lys Thr Gly Ser Leu Trp Lys His Leu Tyr Pro Val His
 85 90 95

Trp Ala Arg Gly Asp Trp Tyr Ser Gly Pro Ala Thr Glu Leu Asp Thr
 100 105 110

Glu Pro Asp Asp Glu Trp Val Lys Asn Arg Lys Asp Glu Ser Arg Ala
 115 120 125

Phe His Glu Trp Asp Glu Asp Ala Asp Ile Asp Glu Ser Glu Glu Ser
 130 135 140

Ala Glu Glu Ser Ile Ala Ile Ser Ile Ala Gln Met Glu Lys Arg Leu
 145 150 155 160

Leu His Gly Leu Ile His Asn Val Leu Pro Tyr Val Gly Thr Ser Val
 165 170 175

Lys Thr Leu Val Leu Ala Tyr Ser Ser Ala Val Ser Ser Lys Met Val
 180 185 190

Arg Gln Ile Leu Glu Leu Cys Pro Asn Leu Glu His Leu Asp Leu Thr
 195 200 205

Gln Thr Asp Ile Ser Asp Ser Ala Phe Asp Ser Trp Ser Trp Leu Gly
 210 215 220

Cys Cys Gln Ser Leu Arg His Leu Asp Leu Ser Gly Cys Glu Lys Ile
 225 230 235 240

Thr Asp Val Ala Leu Glu Lys Ile Ser Arg Ala Leu Gly Ile Leu Thr
 245 250 255

Ser His Gln Ser Gly Phe Leu Lys Thr Ser Thr Ser Lys Ile Thr Ser
 260 265 270

Thr Ala Trp Lys Asn Lys Asp Ile Thr Met Gln Ser Thr Lys Gln Tyr
 275 280 285

Ala Cys Leu His Asp Leu Thr Asn Lys Gly Ile Gly Glu Glu Ile Asp
 290 295 300

Asn Glu His Pro Trp Thr Lys Pro Val Ser Ser Glu Asn Phe Thr Ser
 305 310 315 320

Pro Tyr Val Trp Met Leu Asp Ala Glu Asp Leu Ala Asp Ile Glu Asp
 325 330 335

Thr Val Glu Trp Arg His Arg Asn Val Glu Ser Leu Cys Val Met Glu
 340 345 350

Thr Ala Ser Asn Phe Ser Cys Ser Thr Ser Gly Cys Phe Ser Lys Asp
 355 360 365

Ile Val Gly Leu Arg Thr Ser Val Cys Trp Gln Gln His Cys Ala Ser
 370 375 380

Pro Ala Phe Ala Tyr Cys Gly His Ser Phe Cys Cys Thr Gly Thr Ala
 385 390 395 400

Leu Arg Thr Met Ser Ser Leu Pro Glu Ser Ser Ala Met Cys Arg Lys
 405 410 415

Ala Ala Arg Thr Arg Leu Pro Arg Gly Lys Asp Leu Ile Tyr Phe Gly
 420 425 430

Ser Glu Lys Ser Asp Gln Glu Thr Gly Arg Val Leu Leu Phe Leu Ser
 435 440 445

Leu Ser Gly Cys Tyr Gln Ile Thr Asp His Gly Leu Arg Val Leu Thr
 450 455 460

Leu Gly Gly Leu Pro Tyr Leu Glu His Leu Asn Leu Ser Gly Cys
 465 470 475 480

Leu Thr Ile Thr Gly Ala Gly Leu Gln Asp Leu Val Ser Ala Cys Pro
 485 490 495

Ser Leu Asn Asp Glu Tyr Phe Tyr Cys Asp Asn Ile Asn Gly Pro
 500 505 510

His Ala Asp Thr Ala Ser Gly Cys Gln Asn Leu Gln Cys Gly Phe Arg
 515 520 525

Ala Cys Cys Arg Ser Gly Glu Pro Leu Thr Ser Asp Leu Cys Leu Leu
 530 535 540

His Leu Ala Glu Gln Ala Phe Phe His Ala Leu Tyr Ser His Ile Ser
 545 550 555 560

Cys Val Asn His Pro Phe Leu Ser Val Thr Cys Phe Gly Pro Ile Xaa
 565 570 575

Tyr Asn Phe Arg Asn Leu Asn Tyr Gln Xaa Ile Val Met Leu
 580 585 590

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<210> 53
<211> 1681
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 53
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gagggcaaaa ggagcaactag cttagtcaga gccatgttc aggtcacaat gtgtatgtcag 180
atgttgctta taaatccctt cttgtcttc ccattcttaa atcttgatag gtgcctgtt 240
ggaaactgta aatgccttcc ccaatggaga atcaacagat tgggtgatgg tggagtgg 300
caggaagact caggtcttct agaggaaagg atgcctcata accccctnng cccaggcagc 360
tgctgtcaga gaatgacaca gcacctgcac agtcgctgtc cacttcctgc cactgctgtc 420
ggtggggta cgggagcaaa gttaggcgtgg actttgacat gagggagctg agccccatc 480
cgcttgcgtgc ctgcacgggt aacctgctgg cagtcgtaca gctcgaggcg ctccaggcct 540
cgccaggctct ctaggtgtc cagggccaca tcagtgatgaa ggaggcagtt gtccaactcc 600
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gkgtatgagtt cacagtggaa caggctcagg gcttgcagtt taggacagtg aatggagagc 720
tgatgagtg tgctgtcggt tatcaggatg cawtcttcaa gatccatctt ctccaattcg 780
tgcaattcc gagctaaaag tgtaaaacct gcgtcagtc aatggagca tcgggcagcc 840
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ttgctgcaac ccgaaaggca gagagcctgt agccgggtgac agccccatc tatctgcacc 960
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gcttcaggg ctcgacaaacc tcgcaccagt gcctcgatgc catcctcgat gatctgtatca 1140
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ctgttgtaa tagacacaca ggaggtcaga wccagatgtt tcagtttgc acagaatctg 1260
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ccctctacat ctatttggaa gttaaaaaga tctattttt gccagttgt tccatccagg 1500
gctaagatgt tccaagcctt ggaatctgt gcacatcgcc acaaaggatc tatatccaag 1560
aaggaaaata ttcttaacag aagttctttt gttaactttt tgttaataag gccttcatca 1620
ttgttgtgaga aaaccatggc cgaagagccg cgagcgagcc cacagcccg agtcacacgg 1680
c 1681

<210> 54
<211> 437
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

<400> 54
Arg Val Thr Ser Gly Cys Gly Leu Ala Arg Gly Ser Ser Ala Met Val
    1           5           10          15

Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro Lys Glu
    20          25           30

Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu Cys Arg
    35          40           45

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Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp Gly Ser
 50 55 60

Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Ile Asp Val Glu Gly
 65 70 75 80

Arg Val Val Glu Asn Ile Ser Lys Arg Cys Val Gly Phe Leu Arg Lys
 85 90 95

Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Asp Ser Ser Leu Lys Thr
 100 105 110

Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn Gly Cys
 115 120 125

Thr Lys Ile Thr Asp Ser Thr Cys Tyr Ser Leu Ser Arg Phe Cys Ser
 130 135 140

Lys Leu Lys His Leu Xaa Leu Thr Ser Cys Val Ser Ile Thr Asn Ser
 145 150 155 160

Ser Leu Lys Gly Ile Ser Glu Gly Cys Arg Asn Leu Glu Tyr Leu Asn
 165 170 175

Leu Ser Trp Cys Asp Gln Ile Thr Lys Asp Gly Ile Glu Ala Leu Val
 180 185 190

Arg Gly Cys Arg Gly Leu Lys Ala Leu Leu Leu Arg Gly Cys Thr Gln
 195 200 205

Leu Glu Asp Glu Ala Leu Lys His Ile Gln Asn Tyr Cys His Glu Leu
 210 215 220

Val Ser Leu Asn Leu Gln Ser Cys Ser Arg Ile Thr Asp Glu Gly Val
 225 230 235 240

Val Gln Ile Cys Arg Gly Cys His Arg Leu Gln Ala Leu Cys Leu Ser
 245 250 255

Gly Cys Ser Asn Leu Thr Asp Ala Ser Leu Thr Ala Leu Gly Leu Asn
 260 265 270

Cys Pro Arg Leu Gln Ile Leu Glu Ala Ala Arg Cys Ser His Leu Thr
 275 280 285

Asp Ala Gly Phe Thr Leu Leu Ala Arg Asn Cys His Glu Leu Glu Lys
 290 295 300

Met Asp Leu Glu Xaa Cys Ile Leu Ile Thr Asp Ser Thr Leu Ile Gln
 305 310 315 320

Leu Ser Ile His Cys Pro Lys Leu Gln Ala Leu Ser Leu Ser His Cys
 325 330 335

Glu Leu Ile Xaa Asp Asp Gly Ile Leu His Leu Ser Asn Ser Thr Cys
 340 345 350

Gly His Glu Arg Leu Arg Val Leu Glu Leu Asp Asn Cys Leu Leu Ile
 355 360 365

Thr Asp Val Ala Leu Xaa His Leu Glu Asn Cys Arg Gly Leu Glu Arg

370

375

380

Leu Glu Leu Tyr Asp Cys Gln Gln Val Thr Arg Ala Gly Ile Lys Arg
385 390 395 400

Met Arg Ala Gln Leu Pro His Val Lys Val His Ala Tyr Phe Ala Pro
405 410 415

Val Thr Pro Pro Thr Ala Val Ala Gly Ser Gly Gln Arg Leu Cys Arg
420 425 430

Cys Cys Val Ile Leu
435

<210> 55

<211> 1866

<212> DNA

<213> Homo sapiens

<400> 55

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aacagccaga ctccccctct caatgcagag gttagtccagt atgccaaaga agtagtggat 180
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agagctgtgc tagaactgaa tgcaagctt ccaaaagtgt tcataaaaaa gagctttact 1860
cagtga 1866

<210> 56

<211> 621

<212> PRT

<213> Homo sapiens

<400> 56

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20	25	30	
Asn Thr His Arg Ala Ile Glu Ser Asn Ser Gln Thr Ser Pro Leu Asn			
35	40	45	
Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val Asp Phe Ser Ser His			
50	55	60	
Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met Trp Asn Leu Ala Gly			
65	70	75	80
Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe Thr Gln Thr Ala Val			
85	90	95	
Phe Arg Thr Tyr Gly Thr Trp Trp Asp Gln Cys Pro Ser Ala Ser Leu			
100	105	110	
Pro Phe Lys Arg Thr Pro Pro Asn Phe Gln Ser Gln Asp Tyr Val Glu			
115	120	125	
Leu Thr Phe Glu Gln Gln Val Tyr Pro Thr Ala Val His Val Leu Glu			
130	135	140	
Thr Tyr His Pro Gly Ala Val Ile Arg Ile Leu Ala Cys Ser Ala Asn			
145	150	155	160
Pro Tyr Ser Pro Asn Pro Pro Ala Glu Val Arg Trp Glu Ile Leu Trp			
165	170	175	
Ser Glu Arg Pro Thr Lys Val Asn Ala Ser Gln Ala Arg Gln Phe Lys			
180	185	190	
Pro Cys Ile Lys Gln Ile Asn Phe Pro Thr Asn Leu Ile Arg Leu Glu			
195	200	205	
Val Asn Ser Ser Leu Leu Glu Tyr Tyr Thr Glu Leu Asp Ala Val Val			
210	215	220	
Leu His Gly Val Lys Asp Lys Pro Val Leu Ser Leu Lys Thr Ser Leu			
225	230	235	240
Ile Asp Met Asn Asp Ile Glu Asp Asp Ala Tyr Ala Glu Lys Asp Gly			
245	250	255	
Cys Gly Met Asp Ser Leu Asn Lys Lys Phe Ser Ser Ala Val Leu Gly			
260	265	270	
Glu Gly Pro Asn Asn Gly Tyr Phe Asp Lys Leu Pro Tyr Glu Leu Ile			
275	280	285	
Gln Leu Ile Leu Asn His Leu Thr Leu Pro Asp Leu Cys Arg Leu Ala			
290	295	300	
Gln Thr Cys Lys Leu Leu Ser Gln His Cys Cys Asp Pro Leu Gln Tyr			
305	310	315	320
Ile His Leu Asn Leu Gln Pro Tyr Trp Ala Lys Leu Asp Asp Thr Ser			
325	330	335	

Leu Glu Phe Leu Gln Ser Arg Cys Thr Leu Val Gln Trp Leu Asn Leu
 340 345 350

 Ser Trp Thr Gly Asn Arg Gly Phe Ile Ser Val Ala Gly Phe Ser Arg
 355 360 365

 Phe Leu Lys Val Cys Gly Ser Glu Leu Val Arg Leu Glu Leu Ser Cys
 370 375 380

 Ser His Phe Leu Asn Glu Thr Cys Leu Glu Val Ile Ser Glu Met Cys
 385 390 395 400

 Pro Asn Leu Gln Ala Leu Asn Leu Ser Ser Cys Asp Lys Leu Pro Pro
 405 410 415

 Gln Ala Phe Asn His Ile Ala Lys Leu Cys Ser Leu Lys Arg Leu Val
 420 425 430

 Leu Tyr Arg Thr Lys Val Glu Gln Thr Ala Leu Leu Ser Ile Leu Asn
 435 440 445

 Phe Cys Ser Glu Leu Gln His Leu Ser Leu Gly Ser Cys Val Met Ile
 450 455 460

 Glu Asp Tyr Asp Val Ile Ala Ser Met Ile Gly Ala Lys Cys Lys Lys
 465 470 475 480

 Leu Arg Thr Leu Asp Leu Trp Arg Cys Lys Asn Ile Thr Glu Asn Gly
 485 490 495

 Ile Ala Glu Leu Ala Ser Gly Cys Pro Leu Leu Glu Glu Leu Asp Leu
 500 505 510

 Gly Trp Cys Pro Thr Leu Gln Ser Ser Thr Gly Cys Phe Thr Arg Leu
 515 520 525

 Ala His Gln Leu Pro Asn Leu Gln Lys Leu Phe Leu Thr Ala Asn Arg
 530 535 540

 Ser Val Cys Asp Thr Asp Ile Asp Glu Leu Ala Cys Asn Cys Thr Arg
 545 550 555 560

 Leu Gln Gln Leu Asp Ile Leu Gly Thr Arg Met Val Ser Pro Ala Ser
 565 570 575

 Leu Arg Lys Leu Leu Glu Ser Cys Lys Asp Leu Ser Leu Leu Asp Val
 580 585 590

 Ser Phe Cys Ser Gln Ile Asp Asn Arg Ala Val Leu Glu Leu Asn Ala
 595 600 605

 Ser Phe Pro Lys Val Phe Ile Lys Lys Ser Phe Thr Gln
 610 615 620

<210> 57
 <211> 984
 <212> DNA
 <213> Homo sapiens

<400> 57
 atgcaacttacatgtat agagttcaag attactata cccggcttc agatggtgat 60
 ggcgttggaa acagctacat tgaagataat gatgatgaca gcaaaatggc agatctcttgc 120
 tcctacttcc agcagcaact cacatttcag gagtctgtgc tttaaactgtg tcagcctgag 180
 cttagagagca gtcagattca catatcagtgc ctggcaatgg aggtcctgtat gtacatcttc 240
 cgatgggtgg tgtcttagtgc cttggaccc agatcattgg agcagttgtc gctgggtgtgc 300
 agaggattct acatctgtgc cagagaccct gaaatatggc gtctggctgc cttgaaaagtt 360
 tgccccagaa gctgtattaa acttggcc tacacgtcct ggagagagat gtttttagaa 420
 cggcctcggttgc ttccgtgttat atcgtaaaa ccacatata tctgtcaaggg 480
 gaacagtcttcatatagagcc tggcaccaag tggatattat caggtacata 540
 agattcttc ctgatggcca tggatgtatg ttgacaaccc ctgaagagcc tcagtccatt 600
 gttccacgtt taagaactag gaataccagg actgatgcaa ttctactggg tcaactatcgc 660
 ttgtcacaag acacagacaa tcagacccaa gtatttgcgtg taataactaa gaaaaaagaa 720
 gaaaaaccac ttgactataa atacagatat ttccgtcgat tccagtggc accagaggta caacaaactc 780
 cagagtttc atgtggggct acagctatgt tccagtggc accagaggta caacaaactc 840
 atctggatac atcattcttgc tcacattact tacaatcaa ctggtgagac tgcagtcgt 900
 gctttgaga ttgacaagat gtacaccccc ttgttctcg ccagagtaag gagctacaca 960
 gcttctcag aaaggccctct gtag 984

<210> 58
 <211> 327
 <212> PRT
 <213> Homo sapiens

<400> 58															
Met	Gln	Leu	Val	Pro	Asp	Ile	Glu	Phe	Lys	Ile	Thr	Tyr	Thr	Arg	Ser
1				5					10				15		
Pro	Asp	Gly	Asp	Gly	Val	Gly	Asn	Ser	Tyr	Ile	Glu	Asp	Asn	Asp	Asp
					20				25				30		
Asp	Ser	Lys	Met	Ala	Asp	Leu	Leu	Ser	Tyr	Phe	Gln	Gln	Gln	Leu	Thr
			35				40				45				
Phe	Gln	Glu	Ser	Val	Leu	Lys	Leu	Cys	Gln	Pro	Glu	Leu	Glu	Ser	Ser
					50		55			60					
Gln	Ile	His	Ile	Ser	Val	Leu	Pro	Met	Glu	Val	Leu	Met	Tyr	Ile	Phe
65					70				75				80		
Arg	Trp	Val	Val	Ser	Ser	Asp	Leu	Asp	Leu	Arg	Ser	Leu	Glu	Gln	Leu
						85				90			95		
Ser	Leu	Val	Cys	Arg	Gly	Phe	Tyr	Ile	Cys	Ala	Arg	Asp	Pro	Glu	Ile
				100				105			110				
Trp	Arg	Leu	Ala	Cys	Leu	Lys	Val	Trp	Gly	Arg	Ser	Cys	Ile	Lys	Leu
	115				120					125					
Val	Pro	Tyr	Thr	Ser	Trp	Arg	Glu	Met	Phe	Leu	Glu	Arg	Pro	Arg	Val
	130				135				140						
Arg	Phe	Asp	Gly	Val	Tyr	Ile	Ser	Lys	Thr	Thr	Tyr	Ile	Arg	Gln	Gly
145				150				155			160				
Glu	Gln	Ser	Leu	Asp	Gly	Phe	Tyr	Arg	Ala	Trp	His	Gln	Val	Glu	Tyr
			165				170			175					
Tyr	Arg	Tyr	Ile	Arg	Phe	Phe	Pro	Asp	Gly	His	Val	Met	Met	Leu	Thr
	180				185					190					

Thr	Pro	Glu	Glu	Pro	Gln	Ser	Ile	Val	Pro	Arg	Leu	Arg	Thr	Arg	Asn
195							200						205		
Thr	Arg	Thr	Asp	Ala	Ile	Leu	Leu	Gly	His	Tyr	Arg	Leu	Ser	Gln	Asp
210							215						220		
Thr	Asp	Asn	Gln	Thr	Lys	Val	Phe	Ala	Val	Ile	Thr	Lys	Lys	Glu	
225					230					235				240	
Glu	Lys	Pro	Leu	Asp	Tyr	Lys	Tyr	Arg	Tyr	Phe	Arg	Arg	Val	Pro	Val
	245						250						255		
Gln	Glu	Ala	Asp	Gln	Ser	Phe	His	Val	Gly	Leu	Gln	Leu	Cys	Ser	Ser
	260						265						270		
Gly	His	Gln	Arg	Phe	Asn	Lys	Leu	Ile	Trp	Ile	His	His	Ser	Cys	His
	275						280						285		
Ile	Thr	Tyr	Lys	Ser	Thr	Gly	Glu	Thr	Ala	Val	Ser	Ala	Phe	Glu	Ile
	290						295						300		
Asp	Lys	Met	Tyr	Thr	Pro	Leu	Phe	Phe	Ala	Arg	Val	Arg	Ser	Tyr	Thr
	305						310						315		320
Ala	Phe	Ser	Glu	Arg	Pro	Leu									
						325									

<210> 59
<211> 765
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 59
gcagccctgg atcctgactt agagaatgat gatttctttg tcagaaaagac tggggctttc 60
catgcaaatc catatgttct ccgagcttt gaagacttta gaaagttctc tgagcaagat 120
gattctgttag agcgagatat aattttacag tgttagagaag gtgaacttgt acttccggat 180
ttggaaaaag atgatatgat tggtcgccga atcccagcac agaagaaaaga agtgccgctg 240
tctggggccc cagatagata ccaccagtc cctttccccg aaccctggac tcttcctcca 300
gaaattcaag caaaaattct ctgtgtactt gaaaggacat gcccattccaa agaaaaaaaaagt 360
aatagctgtta gaatatttagt tccttcatat cggcagaaga aagatgacat gctgacacgt 420
aagattcagt cctggaaact gggacttacc gtgcctccca tcagttcac ncctggcccc 480
tgcagtgagg ctgacttgaa gagatggag gccatccggg aggccagcag actcaggcac 540
aagaaaaaggc tgatggtgaa gagactcttt caaaaagattt atggtgagaa tgggagtaag 600
tccatgagtg atgtcagcgc agaagatgtt caaaaacttgc gtcagctgcg ttacgaggag 660
atgcagaaaaaaaataatcaca attaaaagaa caagatcaga aatggcagga tgaccttgca 720
aaatggaaaatcgtcggaaa aagtttacact tcagatctgc agaag 765

<210> 60
<211> 255
<212> PRT
<213> Homo sapiens

<400> 60
Ala Ala Leu Asp Pro Asp Leu Glu Asn Asp Asp Phe Phe Val Arg Lys

1	5	10	15
Thr Gly Ala Phe His Ala Asn Pro Tyr Val Leu Arg Ala Phe Glu Asp			
20	25	30	
Phe Arg Lys Phe Ser Glu Gln Asp Asp Ser Val Glu Arg Asp Ile Ile			
35	40	45	
Leu Gln Cys Arg Glu Gly Glu Leu Val Leu Pro Asp Leu Glu Lys Asp			
50	55	60	
Asp Met Ile Val Arg Arg Ile Pro Ala Gln Lys Lys Glu Val Pro Leu			
65	70	75	80
Ser Gly Ala Pro Asp Arg Tyr His Pro Val Pro Phe Pro Glu Pro Trp			
85	90	95	
Thr Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg			
100	105	110	
Thr Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro			
115	120	125	
Ser Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser			
130	135	140	
Trp Lys Leu Gly Thr Thr Val Pro Pro Ile Ser Phe Thr Pro Gly Pro			
145	150	155	160
Cys Ser Glu Ala Asp Leu Lys Arg Trp Glu Ala Ile Arg Glu Ala Ser			
165	170	175	
Arg Leu Arg His Lys Lys Arg Leu Met Val Glu Arg Leu Phe Gln Lys			
180	185	190	
Ile Tyr Gly Glu Asn Gly Ser Lys Ser Met Ser Asp Val Ser Ala Glu			
195	200	205	
Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile			
210	215	220	
Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala			
225	230	235	240
Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys			
245	250	255	
<210> 61			
<211> 36			
<212> PRT			
<213> Homo sapiens			
<400> 61			
Leu Pro Pro Glu Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr			
1	5	10	15
Asp Leu Cys Leu Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu			
20	25	30	
Leu Leu Trp Gln			

<210> 62
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 62
 Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr
 1 5 10 15

Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu
 20 25 30

Leu Cys Gln Ser Ser Gly Lys Val Trp Lys
 35 40

<210> 63
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 63
 Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala Lys Ala
 1 5 10 15

Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys Val Arg
 20 25 30

Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile
 35 40

<210> 64
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 64
 Leu Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln
 1 5 10 15

Asp Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala
 20 25 30

Asn Asp Pro Asn Leu Trp Lys
 35

<210> 65
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 65
 Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala Tyr Leu His Leu Pro
 1 5 10 15

Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala Trp Tyr Glu Leu Ile

20

25

30

Leu Ser Leu Asp Ser Thr Arg Trp Arg
35 40

<210> 66
<211> 39
<212> PRT
<213> Homo sapiens

<400> 66
Leu Pro Thr Asp Pro Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg
1 5 10 15

Asp Leu Ile Asn Cys Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser
20 25 30

Ser His Asp Pro Leu Trp Arg
35

<210> 67
<211> 40
<212> PRT
<213> Homo sapiens

<400> 67
Leu Pro Glu Pro Leu Leu Leu Arg Val Leu Ala Ala Leu Pro Ala Ala
1 5 10 15

Glu Leu Val Gln Ala Cys Arg Leu Val Cys Leu Arg Trp Lys Glu Leu
20 25 30

Val Asp Gly Ala Pro Leu Trp Leu
35 40

<210> 68
<211> 40
<212> PRT
<213> Homo sapiens

<400> 68
Leu Phe Pro Pro Glu Leu Val Glu His Ile Ile Ser Phe Leu Pro Val
1 5 10 15

Arg Asp Leu Val Ala Leu Gly Gln Thr Cys Arg Tyr Phe His Glu Val
20 25 30

Cys Asp Gly Glu Gly Val Trp Arg
35 40

<210> 69
<211> 44
<212> PRT
<213> Homo sapiens

<400> 69
Leu Pro Glu Val Leu Leu His Met Cys Ser Tyr Leu Asp Met Arg

1 5 10 15

Ala Leu Gly Arg Leu Ala Gln Val Tyr Arg Trp Leu Trp His Phe Thr
20 25 30

Asn Cys Asp Leu Leu Arg Arg Gln Ile Ala Trp Ala
35 40

<210> 70
<211> 40
<212> PRT
<213> Homo sapiens

<400> 70
Leu Pro Leu His Met Leu Asn Asn Ile Leu Tyr Arg Phe Ser Asp Gly
1 5 10 15

Trp Asp Ile Ile Thr Leu Gly Gln Val Thr Pro Thr Leu Tyr Met Leu
20 25 30

Ser Glu Asp Arg Gln Leu Trp Lys
35 40

<210> 71
<211> 39
<212> PRT
<213> Homo sapiens

<400> 71
Leu Pro Asp His Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn
1 5 10 15

Gln Leu Cys Arg Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala
20 25 30

Trp Asp Pro Arg Leu Trp Arg
35

<210> 72
<211> 44
<212> PRT
<213> Homo sapiens

<400> 72
Ile Pro Leu Glu Ile Leu Val Gln Ile Phe Gly Leu Leu Val Ala Ala
1 5 10 15

Asp Gly Pro Met Pro Phe Leu Gly Arg Ala Ala Arg Val Cys Arg Arg
20 25 30

Trp Gln Glu Ala Ala Ser Gln Pro Ala Leu Trp His
35 40

<210> 73
<211> 39
<212> PRT
<213> Homo sapiens

<400> 73
Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu Asn Pro Gln
1 5 10 15

Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser Gln Leu Thr
20 25 30

Lys Thr Gly Ser Leu Trp Lys
35

<210> 74
<211> 39
<212> PRT
<213> Homo sapiens

<400> 74
Leu Pro Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val
1 5 10 15

Thr Leu Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala
20 25 30

Leu Asp Gly Ser Asn Trp Gln
35

<210> 75
<211> 48
<212> PRT
<213> Homo sapiens

<400> 75
Leu Pro Tyr Glu Leu Ile Gln Leu Ile Leu Asn His Leu Thr Leu Pro
1 5 10 15

Asp Leu Cys Arg Leu Ala Gln Thr Cys Lys Leu Leu Ser Gln His Cys
20 25 30

Cys Asp Pro Leu Gln Tyr Ile His Leu Asn Leu Gln Pro Tyr Trp Ala
35 40 45

<210> 76
<211> 44
<212> PRT
<213> Homo sapiens

<400> 76
Leu Pro Met Glu Val Leu Met Tyr Ile Phe Arg Trp Val Val Ser Ser
1 5 10 15

Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu Ser Leu Val Cys Arg Gly
20 25 30

Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile Trp Arg

35

40

<210> 77
<211> 49
<212> PRT
<213> Homo sapiens

<400> 77
Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg Thr
1 5 10 15

Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro Ser
20 25 30

Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser Trp
35 40 45

Lys

<210> 78
<211> 39
<212> PRT
<213> Homo sapiens

<400> 78
Leu Pro His His Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu
1 5 10 15

Asp Arg Ala Cys Ala Ser Ser Val Cys Arg Arg Trp Asn Glu Val Phe
20 25 30

His Ile Ser Asp Leu Trp Arg
35

<210> 79
<211> 43
<212> PRT
<213> Homo sapiens

<400> 79
Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile Ser Ala Leu
1 5 10 15

Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys Gly Ser Trp
20 25 30

Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala
35 40

<210> 80
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

Oligonucleotide

<400> 80
agttagtaaca aaggtaaaag acatgttact gtatcgctga ggatgccttc aattaagtt 59

<210> 81
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 81
gcggttactt acttagagct cgacgtctta cttacttagc tcacttctct tcacacca 58

<210> 82
<211> 12
<212> PRT
<213> Homo sapiens

<400> 82
Cys Asp Gly Glu Lys Asp Thr Tyr Ser Tyr Leu Ala
1 5 10

<210> 83
<211> 25
<212> PRT
<213> Homo sapiens

<400> 83
Cys Glu Ser Ser Phe Ser Leu Asn Met Asn Phe Ser Ser Lys Arg Thr
1 5 10 15

Lys Phe Lys Ile Thr Thr Ser Met Gln
20 25

<210> 84
<211> 12
<212> PRT
<213> Homo sapiens

<400> 84
Cys Glu Glu Ala Gln Val Arg Lys Glu Asn Gln Trp
1 5 10

<210> 85
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> Phosphorylation
<222> 8
<223> Phosothreonine

<400> 85

Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly Leu Arg Arg
1 5 10 15

Arg Gln Thr

<210> 86
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 86
cctggggat gttctca 17

<210> 87
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 87
ggcttccggg catttag 17

<210> 88
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 88
catctggcac gattcca 17

<210> 89
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 89
ccgctcatcg tatgaca 17

<210> 90
<211> 19
<212> PRT
<213> Homo sapiens

<220>

<221> Phosphorylation

<222> 8

<223> Phosotyrosine

<400> 90

Ala Glu Ile Gly Val Gly Ala Tyr Gly Thr Val Tyr Lys Ala Arg Asp
1 5 10 15

Pro His Ser

<210> 91

<211> 20

<212> PRT

<213> Homo sapiens

<220>

<221> Phosphorylation

<222> 9

<223> Phosothreonine

B5
21 <400> 91

Asn Asn Ala Gly Ser Val Glu Trp Thr Pro Lys Lys Pro Gly Leu Arg
1 5 10 15
Arg Arg Gln Thr
20

<210> 92

<211> 15

<212> PRT

<213> Homo sapiens

<400> 92

Gln Ile Tyr Tyr Ser Asp Lys Asp Asp Glu Glu Phe Glu Tyr Arg
1 5 10 15